

# Sonia Garcia

## List of Publications by Year in descending order

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69  
papers

2,360  
citations

172457

29  
h-index

243625

44  
g-index

74  
all docs

74  
docs citations

74  
times ranked

2016  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cytogenetic features of <sc>rRNA</sc> genes across land plants: analysis of the Plant <sc>rDNA</sc> database. <i>Plant Journal</i> , 2017, 89, 1020-1030.	5.7	133
2	Evolutionary trends in animal ribosomal DNA loci: introduction to a new online database. <i>Chromosoma</i> , 2018, 127, 141-150.	2.2	115
3	Plant rDNA database: ribosomal DNA loci information goes online. <i>Chromosoma</i> , 2012, 121, 389-394.	2.2	102
4	Studies on pharmaceutical ethnobotany in the high river Ter valley (Pyrenees, Catalonia, Iberian) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6	4.1	90
5	Biology, Genome Evolution, Biotechnological Issues and Research Including Applied Perspectives in <i>Artemisia</i> (Asteraceae). <i>Advances in Botanical Research</i> , 2011, 60, 349-419.	1.1	75
6	Bâ€chrom: a database on Bâ€chromosomes of plants, animals and fungi. <i>New Phytologist</i> , 2017, 216, 635-642.	7.3	75
7	Linkage of 35S and 5S rRNA genes in <i>Artemisia</i> (family Asteraceae): first evidence from angiosperms. <i>Chromosoma</i> , 2009, 118, 85-97.	2.2	72
8	Genome size dynamics in <i>Artemisia</i> L. (Asteraceae): following the track of polyploidy. <i>Plant Biology</i> , 2010, 12, 820-830.	3.8	68
9	Genome Size Variation in the Genus <i>Carthamus</i> (Asteraceae, Cardueae): Systematic Implications and Additive Changes During Allopolyploidization. <i>Annals of Botany</i> , 2006, 97, 461-467.	2.9	67
10	Repeated reunions and splits feature the highly dynamic evolution of 5S and 35S ribosomal RNA genes (rDNA) in the Asteraceae family. <i>BMC Plant Biology</i> , 2010, 10, 176.	3.6	66
11	Genome size in <i>Echinops</i> L. and related genera (Asteraceae, Cardueae): karyological, ecological and phylogenetic implications. <i>Biology of the Cell</i> , 2004, 96, 117-124.	2.0	65
12	Origin, Diversity, and Evolution of Telomere Sequences in Plants. <i>Frontiers in Plant Science</i> , 2020, 11, 117.	3.6	63
13	Variation of DNA amount in 47 populations of the subtribe Artemisiinae and related taxa (Asteraceae,) Tj ETQq1 1 0,784314 rgBT /Ov	2.0	57
14	Astonishing 35S rDNA diversity in the gymnosperm species <i>Cycas revoluta</i> Thunb. <i>Chromosoma</i> , 2016, 125, 683-699.	2.2	56
15	Dancing together and separate again: gymnosperms exhibit frequent changes of fundamental 5S and 35S rRNA gene (rDNA) organisation. <i>Heredity</i> , 2013, 111, 23-33.	2.6	53
16	Evolutionary and ecological implications of genome size in the North American endemic sagebrushes and allies ( <i>Artemisia</i> , Asteraceae). <i>Biological Journal of the Linnean Society</i> , 0, 94, 631-649.	1.6	51
17	Extensive ribosomal DNA (18S-5.8S-26S and 5S) colocalization in the North American endemic sagebrushes (subgenus <i>Tridentatae</i> , <i>Artemisia</i> , Asteraceae) revealed by FISH. <i>Plant Systematics and Evolution</i> , 2007, 267, 79-92.	0.9	50
18	Chromosome numbers in the tribes Anthemideae and Inuleae (Asteraceae). <i>Botanical Journal of the Linnean Society</i> , 2005, 148, 77-85.	1.6	48

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19	A molecular phylogenetic approach to western North America endemic <i>Artemisia</i> and allies (Asteraceae): Untangling the sagebrushes. <i>American Journal of Botany</i> , 2011, 98, 638-653.	1.7	48
20	Recent updates and developments to plant genome size databases. <i>Nucleic Acids Research</i> , 2014, 42, D1159-D1166.	14.5	47
21	Expression of 5 S rRNA genes linked to 35 S rDNA in plants, their epigenetic modification and regulatory element divergence. <i>BMC Plant Biology</i> , 2012, 12, 95.	3.6	45
22	Genome size variation at constant chromosome number is not correlated with repetitive DNA dynamism in <i>Anacyclus</i> (Asteraceae). <i>Annals of Botany</i> , 2020, 125, 611-623.	2.9	44
23	GSAD: A genome size in the Asteraceae database. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2011, 79A, 401-404.	1.5	43
24	Chromosome counts in Asian <i>Artemisia</i> L. (Asteraceae) species: from diploids to the first report of the highest polyploid in the genus. <i>Botanical Journal of the Linnean Society</i> , 2007, 153, 301-310.	1.6	41
25	Genome size variation and evolution in the family Asteraceae. <i>Caryologia</i> , 2013, 66, 221-235.	0.3	39
26	Higher-order organisation of extremely amplified, potentially functional and massively methylated 5S rDNA in European pikes ( <i>Esox</i> sp.). <i>BMC Genomics</i> , 2017, 18, 391.	2.8	38
27	Ethnobotany of Food Plants in the High River Ter Valley (Pyrenees, Catalonia, Iberian Peninsula): Non-Crop Food Vascular Plants and Crop Food Plants with Medicinal Properties. <i>Ecology of Food and Nutrition</i> , 2009, 48, 303-326.	1.6	37
28	Genome size variation in the <i>Artemisia arborescens</i> complex (Asteraceae, Anthemideae) and its cultivars. <i>Genome</i> , 2006, 49, 244-253.	2.0	36
29	Reconstructing phylogenetic relationships based on repeat sequence similarities. <i>Molecular Phylogenetics and Evolution</i> , 2020, 147, 106766.	2.7	35
30	Plant rDNA database: update and new features. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau063-bau063.	3.0	34
31	Ribosomal DNA, heterochromatin, and correlation with genome size in diploid and polyploid North American endemic sagebrushes ( <i>Artemisia</i> , Asteraceae). <i>Genome</i> , 2009, 52, 1012-1024.	2.0	33
32	Genome size variation from a phylogenetic perspective in the genus <i>Cheirolophus</i> Cass. (Asteraceae): biogeographic implications. <i>Plant Systematics and Evolution</i> , 2007, 264, 117-134.	0.9	28
33	New data on genome size in 128 Asteraceae species and subspecies, with first assessments for 40 genera, 3 tribes and 2 subfamilies. <i>Plant Biosystems</i> , 2013, 147, 1219-1227.	1.6	28
34	The Utility of Graph Clustering of 5S Ribosomal DNA Homoeologs in Plant Allopolyploids, Homoploid Hybrids, and Cryptic Introgressants. <i>Frontiers in Plant Science</i> , 2020, 11, 41.	3.6	28
35	Pandemics and Traditional Plant-Based Remedies. A Historical-Botanical Review in the Era of COVID19. <i>Frontiers in Plant Science</i> , 2020, 11, 571042.	3.6	27
36	Third release of the plant rDNA database with updated content and information on telomere composition and sequenced plant genomes. <i>Plant Systematics and Evolution</i> , 2017, 303, 1115-1121.	0.9	26

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37	Chromosome numbers in some <i>Artemisia</i> (Asteraceae, Anthemideae) species and genome size variation in its subgenus <i>Dracunculus</i> : Karyological, systematic and phylogenetic implications. <i>Chromosome Botany</i> , 2007, 2, 45-53.	0.2	26
38	Remarkable variation of ribosomal DNA organization and copy number in gnetophytes, a distinct lineage of gymnosperms. <i>Annals of Botany</i> , 2019, 123, 767-781.	2.9	23
39	New or rarely reported chromosome numbers in taxa of subtribe Artemisiinae (Anthemideae, Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.6	22
40	Genome size variation in some representatives of the genus <i>Tripleurospermum</i> . <i>Biologia Plantarum</i> , 2005, 49, 381-387.	1.9	19
41	The striking and unexpected cytogenetic diversity of genus <i>Tanacetum</i> L. (Asteraceae): a cytometric and fluorescent in situ hybridisation study of Iranian taxa. <i>BMC Plant Biology</i> , 2015, 15, 174.	3.6	19
42	Impact of dysploidy and polyploidy on the diversification of high mountain <i>Artemisia</i> (Asteraceae) and allies. <i>Alpine Botany</i> , 2016, 126, 35-48.	2.4	19
43	Palynological study of <i>Ajania</i> and related genera (Asteraceae, Anthemideae). <i>Botanical Journal of the Linnean Society</i> , 2009, 161, 171-189.	1.6	18
44	Genome Size Study in the Valerianaceae: First Results and New Hypotheses. <i>Journal of Botany</i> , 2010, 2010, 1-19.	1.2	17
45	Human-like telomeres in <i>Zostera marina</i> reveal a mode of transition from the plant to the human telomeric sequences. <i>Journal of Experimental Botany</i> , 2020, 71, 5786-5793.	4.8	16
46	Swarm of terminal 35S in <i>Cheirolophus</i> (Asteraceae, Centaureinae). <i>Genome</i> , 2012, 55, 529-535.	2.0	15
47	Changes in genome size in a fragmented distribution area: the case of <i>Artemisia crithmifolia</i> L. (Asteraceae, Anthemideae).. <i>Caryologia</i> , 2009, 62, 152-160.	0.3	14
48	Taxonomic and Nomenclatural Rearrangements in <i>Artemisia</i> Subgen. <i>Tridentatae</i> , Including a Redefinition of <i>Sphaeromeria</i> (Asteraceae, Anthemideae). <i>Western North American Naturalist</i> , 2011, 71, 158-163.	0.4	14
49	FISH mapping of 35S and 5S rRNA genes in <i>Artemisia</i> subgenus <i>Dracunculus</i> (Asteraceae): changes in number of loci during polyploid evolution and their systematic implications. <i>Botanical Journal of the Linnean Society</i> , 2013, 171, 655-666.	1.6	14
50	Progress in the study of genome size evolution in Asteraceae: analysis of the last update. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	14
51	SexChrom, a database on plant sex chromosomes. <i>New Phytologist</i> , 2020, 227, 1594-1604.	7.3	14
52	Extraordinary diversity of telomeres, telomerase RNAs and their template regions in Saccharomycetaceae. <i>Scientific Reports</i> , 2021, 11, 12784.	3.3	14
53	Genome size in aquatic and wetland plants: fitting with the large genome constraint hypothesis with a few relevant exceptions. <i>Plant Systematics and Evolution</i> , 2015, 301, 1927-1936.	0.9	13
54	Plastome Diversity and Phylogenomic Relationships in Asteraceae. <i>Plants</i> , 2021, 10, 2699.	3.5	13

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55	Chromosome Numbers in Three Asteraceae Tribes from Inner Mongolia (China), with Genome Size Data for Cardueae. <i>Folia Geobotanica</i> , 2009, 44, 307-322.	0.9	11
56	A genome size and phylogenetic survey of Mediterranean Tripleurospermum and Matricaria (Anthemideae, Asteraceae). <i>PLoS ONE</i> , 2018, 13, e0203762.	2.5	11
57	Analyses of the Updated "Animal rDNA Loci Database" with an Emphasis on Its New Features. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11403.	4.1	11
58	Polyploidy and other changes at chromosomal level and in genome size: Its role in systematics and evolution exemplified by some genera of Anthemideae and Cardueae (Asteraceae). <i>Taxon</i> , 2012, 61, 841-851.	0.7	10
59	Physical mapping of ribosomal DNA and genome size in diploid and polyploid North African Calligonum species (Polygonaceae). <i>Plant Systematics and Evolution</i> , 2015, 301, 1569-1579.	0.9	7
60	First genome size estimations for some eudicot families and genera. <i>Collectanea Botanica</i> , 2010, 29, 7-16.	0.2	7
61	Contribution to the knowledge of genome size evolution in edible blueberries (genus <i>Vaccinium</i> ). <i>Journal of Berry Research</i> , 2020, 10, 243-257.	1.4	5
62	Cytogenetic Characterisation of <i>Artemisia absinthium</i> (Asteraceae, Anthemideae) and Its Polish Endemic var. <i>calcigena</i> . <i>Annales Botanici Fennici</i> , 2010, 47, 477-488.	0.1	4
63	Genome size constancy in Antarctic populations of <i>Colobanthus quitensis</i> and <i>Deschampsia antarctica</i> . <i>Polar Biology</i> , 2020, 43, 1407-1413.	1.2	4
64	<i>Cheirolophus intybaceus</i> (Asteraceae, Centaureinae) o la constancia del valor 2C. <i>Collectanea Botanica</i> , 2009, 28, 7-17.	0.2	3
65	Genome size, chromosome number, and rDNA organisation in Algerian populations of <i>Artemisia herba-alba</i> (Asteraceae), a basic plant for animal feeding facing overgrazing erosion. <i>Anales Del Jardín Botánico De Madrid</i> , 2016, 73, 043.	0.4	2
66	Genome-wide analysis of long terminal repeat retrotransposons from the cranberry <i>Vaccinium macrocarpon</i> . <i>Journal of Berry Research</i> , 2022, 12, 165-185.	1.4	2
67	Contribution to the genome size knowledge of New World species from the Heliantheae alliance (Asteraceae). <i>Plant Biosystems</i> , 2019, 153, 559-568.	1.6	0
68	Can we have it all? Repurposing target capture for repeat genomics. A commentary on: "Aiming off the target: recycling target capture sequencing reads for investigating repetitive DNA". <i>Annals of Botany</i> , 2021, 128, iii-v.	2.9	0
69	Primeras medidas del tamaño del genoma en <i>Carduncellus</i> y los géneros afines <i>Femeniasia</i> y <i>Phonus</i> (Asteraceae, Cardueae), con datos para 21 taxones. <i>Collectanea Botanica</i> , 0, 40, e004.	0.2	0